

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd

# QM protein protein search, using sw model

Run on: January 16, 2003, 16:39:12, Search time 7.29571 Seconds  
(without alignments)  
28 464 Million cell updates/sec

Title: US-09-856-070-16  
Perfect score: 25  
Sequence: 1 EREKE 5

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 112892 seqs, 41476128 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_40.\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	25	100.0	85	1	ITF2_CHICK
2	25	100.0	151	1	SSRP_CHICK
3	25	100.0	152	1	HIF4_XENLA
4	25	100.0	160	1	HIF4_PACHA
5	25	100.0	162	1	HIF4_BACPA
6	25	100.0	163	1	HIF4_BACF3
7	25	100.0	167	1	HIF4_AQUAE
8	25	100.0	174	1	YFUF_BACSU
9	25	100.0	180	1	NEF_HV2N3
10	25	100.0	183	1	ATPE_MAL2U
11	25	100.0	184	1	ATPE_PINTH
12	25	100.0	187	1	R84_METUA
13	25	100.0	194	1	HNF4_DPN5L
14	25	100.0	237	1	HIF2_BACTK
15	25	100.0	247	1	HIF2_SPIPL
16	25	100.0	250	1	ACT8_SOLD2
17	25	100.0	250	1	ACT8_SOLD1
18	25	100.0	258	1	PNK1_THESA
19	25	100.0	261	1	STX7_HUMAN
20	25	100.0	261	1	STX7_MOUSE
21	25	100.0	261	1	STX7_PAT
22	25	100.0	265	1	KIFM_MAFPA
23	25	100.0	271	1	STED_CLOPE
24	25	100.0	284	1	ITF2_BOVIN
25	25	100.0	286	1	ITF2_SHEEP
26	25	100.0	297	1	ITF2_HUMAN
27	25	100.0	298	1	ITF2_PAT
28	25	100.0	300	1	ITF2_MOUSE
29	25	100.0	300	1	ITF2_PABIT
30	25	100.0	301	1	ITF2_CHICK
31	25	100.0	310	1	MEAN_STRGO
32	25	100.0	317	1	HIF3_HAINI
33	25	100.0	330	1	HIF3_STAAU

34	25	100.0	341	1	HIF2_MOUSE
35	25	100.0	346	1	HIF2_XENLA
36	25	100.0	358	1	HIF2_XENLA
37	25	100.0	374	1	HIF3_DROVI
38	25	100.0	375	1	HIF3_DROPS
39	25	100.0	375	1	HIF3_DROST
40	25	100.0	380	1	YXHF_BACSU
41	25	100.0	387	1	YXHF_AKAIN
42	25	100.0	392	1	YXHF_CAFEL
43	25	100.0	428	1	ITF2_PAT
44	25	100.0	436	1	ITF2_YEAST
45	25	100.0	437	1	HIF4_MESAU

## ALIGNMENTS

RESULT 1	ITF2_CHICK	STANDARD:	PRT:	85 AA.
ID	ITF2_CHICK	AC	Q90683	
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
GI	16521 2001 (Rel. 43, Last annotation update)			
DE	Transcription factor 4 (Class A helix-loop-helix transcription factor			
DE	GE2) (Fragment).			
GN	TCF4.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves, Neognathae, Galliformes, Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RF	[1]			
RN	SEQUENCE FROM N.A.			
RC	TISSUE=Neural tube;			
PX	MEDLINE=94084260; PubMed=8261111;			
KA	Neuman T., Keen A., Knapik E., Shain D., Ross M., Nornes H.O.,			
RA	Zuber M.X.;			
RT	"MEI and GEI, basic helix-loop helix transcription factors expressed			
RT	at high levels in the developing nervous system and in			
RT	morphogenetically active regions.";			
KC	Eur. J. Neurosci. 5:311-318(1993).			
CC	FUNCTION: TRANSSCRIPTION FACTOR THAT BINDS TO THE IMMUNOGLOBULIN			
CC	ENHANCER MOTIF/KNES-MOTIF. BINDS TO THE E-BOX PRESENT IN THE			
CC	S-MATHEMATIN PEPTIDE 2 INITIATOR ELEMENT (SSTR2-1NF) TO ACTIVATE			
CC	TRANSCRIPTION (BY SIMILARITY).			
CC	SUBUNIT: EFFICIENT DNA BINDING DIMERIZATION WITH ANOTHER			
CC	BHLH PROTEIN. FORMS HOMODIMER OR HETERODIMERS WITH MYOGENIN.			
CC	LOCUS: LOCUS IN CHROMOSOME 1, NUCLEAR (PROBABLY).			
CC	SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF			
CC	TRANSCRIPTION FACTORS.			
CC	THIS SWISS PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by scientific institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/</a> or			
CC	send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
DR	EMBL: J15054; AAA78932.1; -			
DR	InterPro: IP001092; HLF_Basic.			
DR	Tram: P00010; HLF: 1			
DR	SMART: SM00353; HLF: 1			
DE	PROSITE: PS00048; HLF1: 1.			
DR	PROSITE: PS00888; HLF2: 1.			
KW	Transcription regulation, DNA binding, Activator, Nuclear protein.			
FT	NCN_PEP 1			
FT	DNA_BIND 7 19			
FT	DOMAIN 20 61			
FT	DOMAIN 62 85			
FT	NCN_PEP 85 85			
FT	SEQUENCE 85 AA; 10056 MW; 03494874-H00600 CR604;			

DR PROSITE; PS01317; SSRP; 1.  
KW RNA binding; Complete proteome.  
SQ SEQUENCE 151 AA; 17449 MW; 01B229CA79F7562 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 151;  
Best Local Similarity 100.0%; Pred. No. 70; 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5  
|||||  
DB 135 EREKE 139

RESULT 3  
HTF4\_XENIA STANDARD; PRI: 152 AA.  
AC Q91605;  
DI 30-MAY-2000 (Rel. 39, Created)  
DI 30-MAY-2000 (Rel. 39, Last sequence update)  
DI 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Transcription factor Xf1.1 (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
OC Xenopodidae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN |||||  
RP SEQUENCE FROM N.A.  
RC TISSUE=Head;  
EX MEDLINE-96096542; PubMed-8522197;  
RA Shain D.H., Zuber M.X.;  
RT Identification of non-tissue-specific helix-loop-helix genes in  
RT Xenopus laevis.  
RL Gene 165319 320(1995).  
CC -!- FUNCTION: BINDS SPECIFICALLY TO OLIGOMERS OF E-BOX MOTIFS. MAY  
CC PLAY IMPORTANT ROLES DURING DEVELOPMENT OF THE NERVOUS SYSTEM AS  
CC WELL AS IN OTHER ORGAN SYSTEMS (BY SIMILARITY).  
CC -!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER  
CC BHLH PROTEIN. FORMS HOMO- OR HETERO-OLIGOMERS WITH MYOGENIN, E12  
CC AND ITF2 PROTEINS (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
CC TRANSCRIPTION FACTORS.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announcement/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL: U25959; AAA92047.1; -;  
DR InterPro: IPR001092; HLH\_basic.  
DR Pfam: PF00010; HLH; 1.  
DR SMART: SM00453; HLH; 1.  
DR PROSITE; PS00038; HLH.1; 1.  
DR PROSITE; PS00888; HLH.2; 1.  
KW Transcription regulation; DNA-binding; Nuclear protein;  
KW Developmental protein.  
FT NUNTER 1 1  
FT DNA\_BIND 47 59 BASIC DOMAIN.  
FT DOMAIN 60 101 HLH1-LOOP-HELIX MOTIF (BY SIMILARITY).  
FT DOMAIN 102 125 CLASS A SPECIFIC DOMAIN.  
SQ SEQUENCE 152 AA; 17455 MW; 35138AF36552600C CRC64;

Query Match 100.0%; Score 25; DB 1; Length 152;  
Best Local Similarity 100.0%; Pred. No. 71; 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5  
|||||  
DB 43 EREKE 47

DR PROSITE; PS01317; SSRP; 1.  
KW RNA binding; Complete proteome.  
SQ SEQUENCE 151 AA; 17449 MW; 01B229CA79F7562 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 85;  
Best Local Similarity 100.0%; Pred. No. 39;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5  
|||||  
DB 5 EREKE 7

RESULT 2  
SSRP\_CHILN STANDARD; PRI: 151 AA.  
AC Q928K1; Q9JQJ4; Q9K272;  
DI 30-MAY-2000 (Rel. 39, Created)  
DI 30-MAY-2000 (Rel. 39, Last sequence update)  
DI 16-OCT-2001 (Rel. 40, Last annotation update)  
DE SsrA-binding protein.  
DE SMPB OR CPN0437 OR CP0421.  
OS Chlamydia pneumoniae (Chlamydia pneumoniae).  
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia; Chlamydia.  
OX NCBI\_TaxID=83558;  
RN |||||  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
EX MEDLINE-99206606; PubMed-10142388;  
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,  
RA Olinger L., Greenwood J., Davis R.W., Stephens R.S.;  
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis".  
RT Nat. Genet. 21:485-489(1999).  
RL [2]  
CC SEQUENCE FROM N.A.  
CC STRAIN=AR49;  
CC MEDLINE-20150255; PubMed-10684935;  
CC Read I.D., Hunkler K.C., Shen C., Gill S., Heideberg J.F.,  
CC White O., Hickey E.K., Peterson T., Hutterback T., Berry K., Bass S.,  
CC Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson P.,  
CC Gwin M., Nelson W., DeBoy R., Kelcey J., McClarty G., Salzberg S.L.,  
CC Fison J., Fraser C.M.;  
CC "Genome sequences of Chlamydia trachomatis Mogen and Chlamydia  
CC pneumoniae AR49".  
CC Nucleic Acids Res. 28:1497-1406(2000).  
RL [3]  
CC SEQUENCE FROM N.A.  
CC STRAIN=J1148;  
CC MEDLINE-20130349; PubMed-10871362;  
CC Shirai M., Hirakawa H., Kimoto M., Iabuchi M., Kishi F., Ouchi K.,  
CC Shiba T., Ishii K., Hattori M., Kubara S., Nakazawa T.;  
CC "Comparison of whole genome sequences of Chlamydia pneumoniae J1148  
CC from Japan and whole genome sequences of Chlamydia pneumoniae J1148  
CC from Japan and whole genome sequences of Chlamydia pneumoniae J1148  
CC Nucleic Acids Res. 28:2311-2314(2000).  
CC -!- FUNCTION: BINDS SPECIFICALLY TO THE SSRP RNA (1MRNA) AND IS  
CC REQUIRED FOR STABLE ASSOCIATION OF SSRP WITH RIBOSOMES (BY  
CC SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
CC -!- SIMILARITY: BELONGS TO THE SSRP FAMILY.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announcement/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL: AE001618; AAD18486.1; -;  
EMBL: AE002203; AAF48264.1; ALT\_INIT.  
EMBL: AP002546; BAA98547.1; -;  
I03K; CP0421; -;  
DR InterPro: IPR000037; SmpA.  
DR Pfam: PF01668; SmpA; 1.  
DR ProDom: PD0004488; SmpA; 1.  
DR TIGRFAMs: TIGR000086; smpA; 1.

```

RESULT 4
ID HIF4_PAPHA STANDARD: PRT: 160 AA
AC Q28772:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Transcription factor 12 (transcription factor HIF4) (E-box-binding
DE protein) (DNA-binding protein HIF4) (Fragment).
GN TCF12 OR HIF4
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota, Metazoa, Chordata, Vertebrata, Euteleostomi,
OC Mammalia, Eutheria, Primates, Catarrhini, Cercopithecoidea,
OC Cercopitheciinae, Papio.
OX NCBI_TaxID: 9557;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Di Rocco G., Pennuto M., Ili R., Gani N., Filocamo G., Trani E.,
RA Rinaldi A.M., Possenti R., Mandolesi G., Sirinian M.F., Jucker R.,
RA Levi A., Nasi S.;
RT "Interplay of the E box, the cyclic AMP response element, and
RT HIF4/HEB in transcriptional regulation of the neurospecific,
RT neurotrophin-inducible vgf gene."
RL Mol. Cell Biol. 17:1244-1253(1997)
CC -!- FUNCTION: BINDS SPECIFICALLY TO OLIGOMERS OF E-BOX MOTIFS, AND IN
CC PARTICIPATE THE VGF PROMOTER E-BOX MAY PLAY IMPORTANT ROLES DURING
CC DEVELOPMENT OF THE NERVOUS SYSTEM AS WELL AS IN OTHER ORGAN
CC SYSTEMS.
CC -!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
CC HEB PROTEIN, FORMS HOMO- OR HETERO-OLIGOMERS WITH MYOGENIN, E12
CC AND ITP2 PROTEINS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X97234; CAA65873.1; -
CC InterPro: IPR001392; HLH_basic
CC Pfam: PF00010; HLH: 1
CC SMART: SM00353; HLH: 1
CC PROSITE: PS00038; HLH_1: 1.
CC PROSITE: PS50888; HLH_2: 1
CC Transcription regulation; DNA-binding; Nuclear protein;
CC Developmental protein.
CC NON_TER 1
CC FT DNA_BIND 55 67 BASIC DOMAIN.
CC FT DOMAIN 68 109 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
CC FT DOMAIN 110 133 CLASS A SPECIFIC DOMAIN.
CC SQ SEQUENCE 160 AA: 18101 MW: 4870037419AFA395 GPC64;
Query Match 100.0%; Score 25; DB 1; Length 160;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EREKE 5
Db 51 EREKE 55
RESULT 5
ATP6_BACCA STANDARD: PRT: 162 AA.
ID ATP6_BACCA
AC Q28721:
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE ATP synthase B chain precursor (EC 3.6.3.14).
DE ATP synthase B chain precursor (EC 3.6.3.14).
GN ATP6.
OS Bacillus PS3 (Thermophilic bacterium PS-3).
OC Bacteria, Firmicutes, Bacillales, Bacillaceae; Bacillus.
OX NCBI_TaxID: 70306;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=86163679; PubMed=2894854;
RA Ohta S., Yoshida M., Ishizuka M., Hirata H., Hamamoto T.,
RA Ohtawa-Hamamoto Y., Matsuda K., Kojima Y.;
RT "Sequence and over-expression of subunits of adenosine triphosphate
RT synthase in thermophilic bacterium PS3."
RL Biochim Biophys Acta 933:141-155(1988)
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) -> ADP + phosphate +
CC H(+) (Out).
CC -!- SUBUNIT: P-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -!- SIMILARITY: BELONGS TO THE ATPASE B CHAIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC FMR1: D48057; BAA07245.1; -
CC InterPro: IPR002146; ATPsynth_B/B' sub.
CC Pfam: PF00430; ATP-synth_B: 1.
CC TIGRFAMs: TIGR01144; ATP_synth_b: 1.
CC KW Hydrogen ion transport, Transmembrane, CF(0).
CC FT TRANSMEM 16 POTENTIAL.
CC SQ SEQUENCE 162 AA: 18568 MW: A75BP410041C388 GPC64;
Query Match 100.0%; Score 25; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EREKE 5
Db 125 EREKE 129
RESULT 6
ATP6_BACP3 STANDARD: PRT: 163 AA.
ID ATP6_BACP3
AC P09221:
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE ATP synthase B chain precursor (EC 3.6.3.14).
DE ATP synthase B chain precursor (EC 3.6.3.14).
GN ATP6.
OS Bacillus PS3 (Thermophilic bacterium PS-3).
OC Bacteria, Firmicutes, Bacillales, Bacillaceae; Bacillus.
OX NCBI_TaxID: 70306;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=86163679; PubMed=2894854;
RA Ohta S., Yoshida M., Ishizuka M., Hirata H., Hamamoto T.,
RA Ohtawa-Hamamoto Y., Matsuda K., Kojima Y.;
RT "Sequence and over-expression of subunits of adenosine triphosphate
RT synthase in thermophilic bacterium PS3."
RL Biochim Biophys Acta 933:141-155(1988)
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) -> ADP + phosphate +
CC H(+) (Out).
CC -!- SUBUNIT: P-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -!- SIMILARITY: BELONGS TO THE ATPASE B CHAIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC FMR1: D48057; BAA07245.1; -
CC InterPro: IPR002146; ATPsynth_B/B' sub.
CC Pfam: PF00430; ATP-synth_B: 1.
CC TIGRFAMs: TIGR01144; ATP_synth_b: 1.
CC KW Hydrogen ion transport, Transmembrane, CF(0).
CC FT TRANSMEM 16 POTENTIAL.
CC SQ SEQUENCE 163 AA: 18568 MW: A75BP410041C388 GPC64;
Query Match 100.0%; Score 25; DB 1; Length 163;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EREKE 5
Db 125 EREKE 129

```

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: X07804; CAA30650.1;  
 DR PIR: S01499; S01399;  
 DR InterPro: IPR002146; ATPsynl\_B/B'sub.  
 DR Pfam: PF00430; ATP-synth\_B; 1.  
 DR TIGRFAMs: TIGR01144; ATP\_synth\_b; 1.  
 KW Hydrogen ion transport; Transmembrane; CF(0).  
 FT PROPEP 1 11  
 FT CHAIN 12 163 ATP SYNTHASE B CHAIN.  
 FT TRANSMEM 16 36 POTENTIAL.  
 SQ SEQUENCE 163 AA: 18560 MW: 1987900CAUFEFWACF CRC64;

Query Match 100.0%; Score 25; DB 1; Length 163;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5  
 |||||  
 DB 125 SPEKE 129

## RESULT 7

YFBL\_AQUAE  
 ID YFBL\_AQUAE STANDARD: PRT: 167 AA.  
 AC 067521;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein AQ\_1581.  
 GN AQ\_1581.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificae (class); Aquificae; Aquificaceae;  
 OA Aquifex.  
 CX NCBL\_TaxID=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-VF5;  
 RX MEM1NF-98196566; PubMed=9537320;  
 RA Beckert G., Warren P.V., Gaasterland T., Young W.G., Genay A.L.,  
 RA Graham D.E., Overbeek R., Speed M.A., Keller M., Aulay M., Huber P.,  
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RA "The complete genome of the hyperthermophilic bacterium Aquifex  
 aeolicus.";  
 RA Nature 392:353-358(1998).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: AE000746; AAC07489.1;  
 DR Hypothetical protein; Transmembrane; Complete proteome.  
 FT TRANSMEM 5 27 POTENTIAL.  
 SQ SEQUENCE 167 AA: 20031 MW: 21642363AG4554 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 167;  
 Best Local Similarity 100.0%; Pred. No. 78;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5  
 |||||  
 DB 73 EREKE 77

## RESULT 8

YPUF\_BACSU  
 ID YPUF\_BACSU STANDARD: PRT: 174 AA.  
 AC P17617;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Hypothetical protein ypuF (ORF46).  
 GN YPUF.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 CX NCBL\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-168 / Marburg;  
 RX MEDLINE-95020538; PubMed-7948429;  
 RA Sorokin A.V., Zumbstein E., Azevedo V., Ehrlich S.D., Serror P.;  
 RA "The organization of the Bacillus subtilis 168 chromosome region  
 between the spoVA and spoA genetic loci, based on sequence data.";  
 RA Mol. Microbiol. 10:485-495(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-168 / Shew;  
 RA Mironov V.N.;  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-168;  
 RX MEDLINE-98044033; PubMed-9384377;  
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Boursier L., Brans A., Braun M., Briganti S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell R., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Connerion I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita Y., Fujita Y., Fuma S., Galizzi A., Gallion N.,  
 RA Shim S.Y., Glasgow P., Goffeau A., Gollightly E.J., Grand G.,  
 RA Giuseppe G., Guy R.J., Haga K., Haiech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Iwaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinis S., Laubet J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauch C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,  
 RA Noone D., O'Leilly M., Ogawa K., Ogiwara A., Oudea B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Presecan E., Fujic F., Furtelle B., Rapoport G., Pey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Roche E., Roche R., Rose M., Sadate Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Serror S.J., Serror P., Shin B.S., Soldo H.,  
 RA Sorokin A., Taccioni E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpsira P., Tononi A.,  
 RA Totsuka V., Uchiyama S., Vandenbol M., Vannier F., Vassartoli A.,  
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzsaecker T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Zumbstein A.;  
 RA "The complete genome sequence of the Gram-positive bacterium Bacillus  
 subtilis.";  
 RA Nature 390:249-256(1997).

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: L09228; AAA67486.1;  
 DR EMBL: X51510; CAA35883.1;

```

DR EMBL: Z99116; CAB14255.1; -
DR PIR: S4554R; s4554R
DR Subtilisin; HG10523; ypuF.
KW Hypothetical protein, Serine protease.
SQ SEQUENCE 174 AA; 21421 MW; 2068cP4P0R2PRAE CR04;

Query Match 100.0%; Score 25; DB 1; Length 174;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
DB 161 EREKE 165

RESULT 9
NEF_HV2N/
ID NEF_HV2N/ STANDARD; PRT; 180 AA.
AC P05960.
DT 01-NOV-1998 (Rel. 09, Created)
DI 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Negative factor (F-protein) (27 kDa protein) (3'ORF).
GN NEF.
OS Human immunodeficiency virus type 2 (isolate HIR-2) (HIV-2).
OC Viruses; Retrov. viruses; Retroviridae; Lentivirus
OC NCBI_TaxID=11719.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=68420459; PubMed=646162;
RA Zaquy J F., Franchini G., Reliz M. S. Jr., Collalti F., Starcich B.R.,
RA Hall L., Fargnoli K., Jagodzinski L.L., Guo H.-G., Laine F.,
RA Arya S.K., Josephs S.F., Zagury D., Wong-Staal F., Gallo R.C.,
RT "Genetic variability between isolates of human immunodeficiency virus
RT (HIV) type 2 is comparable to the variability among HIV type 1."
RL Proc. Natl. Acad. Sci. U.S.A. 85:5941-5945(1988).
CC -!- FUNCTION: NEF has GTPase, GTP-binding and autophosphorylating
CC activities. It seems to down-regulate the CD4(T4) antigen.
CC
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: J03654; AAR00762.1; -
DR DR
DR HIV: J03654; NEFS2NTHZ.
DR InterPro: IPR001558; HIV_Nef
DR Pfam: PF00469; F-protein; 1.
DR ProDom: PD000031; HIV_Nef; 1.
DR AIDS; Myristate; HIV_Nef; 1.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
SQ SEQUFNFE 180 AA; 20406 MW; 0208E7RAEY267887 CR04;

Query Match 100.0%; Score 25; DB 1; Length 180.
Best Local Similarity 100.0%; Pred. No. 84;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPEKE 5
DB 76 EREKE 80

RESULT 10
ATP_MAIZE
ID ATP_MAIZE STANDARD; PRT; 183 AA.
AC P48186;
DT 01-FEB-1996 (Rel. 33, Created)
DI 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase B chain (EC 3.6.3.14) (Subunit I).
GN ATP.
OS Zea mays (Maize).
OC Chloroplast.
OC NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95395841; PubMed=7666415;
RA Maier R.M., Nuckermann K., Jolani G.B., Koessel H.;
RT "Complete sequence of the maize chloroplast genome: gene content,
RT hotspots of divergence and fine tuning of genetic information by
RT transcript editing."
RL J. Mol. Biol. 251:614-628(1995).
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(in) -> ADP + phosphate +
CC H(+)(out).
CC
CC -!- SUBUNIT: F-TYPE ATPASES HAVE 2 SUBUNITS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
CC HAS THREE MAIN SUBUNITS: A, B AND C.
CC -!- CELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -!- SIMILARITY: BELONGS TO THE ATPASE B CHAIN FAMILY.
CC
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X86563; CAA60382.1; -
DR MaizeDB; 106206; -
DR InterPro: IPR002146; ATPsynth_B/B'sub.
DR Pfam: PF00430; ATP-synth_B; 1.
DR Hydrophob. ion transport; Transmembrane; CF(0); Chloroplast.
FT TRANSMEM 27 45 POTENTIAL.
SQ SEQUENCE 183 AA; 20781 MW; 3748C90129511bCA CR04;

Query Match 100.0%; Score 25; DB 1; Length 183;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5
DB 104 EREKE 108

RESULT 11
ATP_PINH
ID ATP_PINH STANDARD; PRT; 184 AA.
AC Q62939;
DT 15-DEC-1998 (Rel. 37, Created)
DI 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ATP synthase B chain (EC 3.6.3.14) (Subunit I).
GN ATP.
OS Pinus thunbergii (Green pine) (Japanese black pine).
OC Chloroplast.
OC NCBI_TaxID=3350;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95024047; PubMed=7937893;
RA Wakasugi T., Tsudzuki T., Ito S., Nakashima K., Tsudzuki T.,
RA Sugita M.;
RT "Loss of all ndh genes as determined by sequencing the entire
RT chloroplast genome of the black pine Pinus thunbergii."
RL Proc. Natl. Acad. Sci. U.S.A. 91:4794-4798(1994).
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(in) -> ADP + phosphate +
CC H(+)(out).
CC

```

HSSP: P81286; 1C05.  
 11GR: MJ0190; -.  
 InterPro: IPR001912; Ribosomal\_S4.  
 InterPro: IPR003943; S4.  
 Pfam: PF01479; S4; 1.  
 SMART: SM00663; S4; 1.  
 11GRFAMS: 11GR01018; rpsLarch; 1.  
 PROSITE: PS00632; RIBOSOMAL\_S4; 1.  
 Rfam: rfam01018; rRNA-binding; Complete proteome.  
 FEI DOMAIN 105 152 RNA-BINDING (S4 TYPE).  
 SEQUENCE 187 AA; 22650 MB; 7D4C51389D5C8A12 CRC64:

Query Match 100.0%; Score 25; DB 1; Length 187;  
 Best Local Similarity 100.0%; Pred. No. 88;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPEKE 5  
 DB 25 EPEKE 29

RESULT 13  
 HUNB\_DROSIL STANDARD; PRT; 196 AA.  
 04525; 046257;  
 16-OCT-2001 (Rel. 40, Created)  
 16-OCT-2001 (Rel. 40, Last sequence update)  
 16-OCT-2001 (Rel. 40, Last annotation update)  
 Hunchback protein (Fragments).  
 HB.  
 Drosophila silvestris (Fruit fly).  
 OOS  
 Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID:47010;  
 [1]  
 SEQUENCE FROM N.A.  
 Baker R.H., Desalici R.;  
 "Multiple sources of character information and the phylogeny of  
 Hawaiian Drosophilids";  
 Syst. Biol. 46:654-673(1997).  
 -1- FUNCTION: GAP CLASS SEGMENTATION PROTEIN THAT CONTROLS DEVELOPMENT  
 OF HEAD STRUCTURES (BY SIMILARITY).  
 -1- SUBCELLULAR LOCATION: Nuclear (by similarity).  
 -1- SIMILARITY: BELONGS TO THE HUNCHBACK FAMILY OF C2H2-TYPE ZINC-  
 FINGER PROTEINS.

This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/annouce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

EMBL: U93020; AAC03268.1; -;  
 EMBL: U93021; AAC03269.1; -;  
 FlyBase: FB0003422; Ds11vbb.  
 Developmental protein; Gap protein; Zinc-finger;  
 Metal-binding; DNA-binding; Repeat; Nuclear protein.  
 NON\_TER 1 1  
 FT DOMAIN 17 26 POLY-HIS.  
 FT DOMAIN 68 81 POLY-GLN.  
 FT NON\_CONS 102 103  
 FT DOMAIN 126 132 POLY-TBR.  
 FT DOMAIN 134 137 POLY-ALA.  
 FT NON\_TER 196 196  
 SEQUENCE 196 AA; 21523 MB; 30DE5945301AAC78 TAC64:

Query Match 100.0%; Score 25; DB 1; Length 196;  
 Best Local Similarity 100.0%; Pred. No. 92;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5  
DB 177 EREKE 181

## RESULT 14

RP28\_BACTK STANDARD: PPT: 247 AA  
AC P26765;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DE RNA polymerase sigma-28 factor precursor  
OS Bacillus thuringiensis (subsp. kurstaki)  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=29339;  
PN 111  
RP SEQUENCE FROM N.A. AND SEQUENCE OF 20-37  
RC STRAIN:HD-1-Dippe1;  
RX MEDLINE:91267651; PubMed:1004869;  
RA Adams L.F., Brown K.J., Whiteley H.R.;  
RT "Molecular cloning and characterization of two genes encoding sigma  
factors that direct transcription from a Bacillus thuringiensis  
crystal protein gene promoter.";  
RL J. Bacteriol. 174:3846-3854(1994)  
RN [2]  
CC CHARACTERIZATION.  
RX MEDLINE:91072211; PubMed:1701426;  
RA Brown K.L., Whiteley H.R.;  
RT "Isolation of the second Bacillus thuringiensis PNA polymerase that  
transcribes from a crystal protein gene promoter.";  
PC J. Bacteriol. 172:6682-6688(1990).  
CC -!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES  
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND  
THEN IS RELEASED. THIS SIGMA FACTOR DIRECTS TRANSCRIPTION OF  
CRYSTAL PROTEIN GENES. A SPOULATION-REGULATED EVENT.  
CC -!- DEVELOPMENTAL STAGE: IS PROBABLY ACTIVATED AT THE TIME IMMEDIATELY  
PRECEDING SPORE CORTEX FORMATION (STAGE IV).  
CC -!- PTM: ONLY BECOMES ACTIVE AFTER THE PROPEPTE IS REMOVED (PROBABLY  
BY A SPOILIGA ANALOG) (HY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY.  
CC  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL Outstation  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
CC  
DR EMBL: X56696; CAA40024.1; -;  
DR PIP: A30441; A30441;  
DR HSSP: P00579; ISIG.  
DR InterPro: IPR000443; Sigma\_70  
DR Pfam: PF00140; sigma70; 1.  
DR PRINTS: PR00046; SIGMA70PCT  
DR PROSITE: PS00715; SIGMA70.1; 1.  
DR PROSITE: PS00716; SIGMA70.2; 1  
KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;  
FT DNA binding; Sporulation.  
FT PROPEP 1 19  
FT CHAIN 20 247 RNA POLYMERASE SIGMA-28 FACTOR  
FT DOMAIN 77 90 POLYMERASE CORE BINDING (POTENTIAL).  
FT DNA\_BIND 197 206 H-T-H MOTIF (HY SIMILARITY).  
SQ SEQUENCE 237 AA; 27136 MW; CID8E4FB637CEDA5 CRC64;

Query Match 100.0%; Score 25; DB 1; Length 237;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5  
DB 177 EREKE 181

## RESULT 15

RP28\_SPIPL STANDARD: PPT: 247 AA.  
AC P34828;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Elongation factor is (EF-Ts) (Fragment).  
GN TSP.  
OS Spirulina platensis.  
OC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.  
OX NCBI\_TaxID=1156;  
RN 111  
RP SEQUENCE FROM N.A.  
RX MEDLINE:92215147; PubMed:2108895;  
RA Sanangelantoni A.M., Falgout P.C., Ruffarelli F.P., Gualeczi C.O.,  
Tiboni O.;  
RT "Organization and nucleotide sequence of the genes for ribosomal  
protein S2 and elongation factor Ts in Spirulina platensis.";  
RL FEMS Microbiol. Lett. 54:141-145(1990).  
CC -!- FUNCTION: ASSOCIATES WITH THE EF-TU GTP COMPLEX AND INDUCES THE  
EXCHANGE OF GDP TO GTP. IT REMAINS BINDING TO THE AMINOACYL-TRNA  
EF-TU GTP COMPLEX UP TO THE GTP HYDROLYSIS STAGE ON THE RIBOSOME.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: BELONGS TO THE EF-TS FAMILY.  
CC  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL Outstation  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch))  
CC  
DR EMBL: X53651; CAA37701.1; -;  
DR HSSP: P02997; LEPU.  
DR InterPro: IPR001816; EF\_TS.  
DR InterPro: IPR000449; UBA\_domain.  
DR Pfam: PF00627; UBA; 1.  
DR Pfam: PF00889; EF\_TS; 1.  
DR TIGRfam: TIGR00116; tsf; 1.  
DR PROSITE: PS01126; EF\_TS\_1; 1.  
DR PROSITE: PS01127; EF\_TS\_2; 1.  
KW Elongation factor; Protein biosynthesis.  
FT SITE 82 85 INVOLVED IN MG++ ION DISLOCATION FROM EF-  
TU (BY SIMILARITY).  
FT NON\_TER 247 247  
SQ SEQUENCE 247 AA; 25997 MW; BDFE5E82198871ED CRC64;

Query Match 100.0%; Score 25; DB 1; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EREKE 5  
DB 202 EREKE 206

Search completed: January 16, 2003, 16:51:07  
Job time : 8.28571 secs

